



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

In re patent application of

David W. LEUNG et al.

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE
WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter; and

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

5 August 1997
Date

Stephen A. Bent
Stephen A. Bent
Reg. No. 29,768

FOLEY & LARDNER
Suite 500
3000 K Street, N.W.
Washington, D.C. 20007-5109
(202) 672-5300

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LEUNG, David W.
TOMPKINS, Christopher K.
- (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Foley & Lardner
 - (B) STREET: 3000 K Street, N.W., Suite 500
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/842,827
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENT, Stephen A.
 - (B) REGISTRATION NUMBER: 29,768
 - (C) REFERENCE/DOCKET NUMBER: 77319/125
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)672-5300
 - (B) TELEFAX: (202)672-5399
 - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1563 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 342..1193
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 342..1193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGTGGGAG AGAGCGCCCG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGCCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC	120

GAGTGTTCGC	GGGGGCTGTG	AGGGGAGGGC	CCCGGGCGCC	ATTGCTGGCG	GTGGGAGCGC	180
CGCCCGGTCT	CAGCCCGCCC	TCGGCTGCTC	TCCTCCTCCG	GCTGGGAGGG	GCCGTATCTC	240
GGGGCCGTCG	CCAGCCCCGG	CCCGGGCTCG	ATAATCAAGG	GCCTCGGCCG	TCGTCCCGCA	300
CCTCATTTCCA	TCGCCCTTGC	CGGGCAGCCC	GGGCAGAGAC	C ATG TTT GAC AAG	Met Phe Asp Lys	353
				1		
ACG CGG CTG	CCG TAC GTG	GCC CTC GAT	GTG CTC TGC	GTG TTG CTG	GCT	401
Thr Arg Leu	Pro Tyr Val	Ala Leu Asp	Val Leu Cys	Val Leu Leu	Ala	
5	10	15	20			
GGA TTG CCT	TTT GCA ATT	CTT ACT TCA	AGG CAT ACC	CCC TTC CAA	CGA	449
Gly Leu Pro	Phe Ala Ile	Leu Thr Ser	Arg His Thr	Pro Phe Gln	Arg	
	25	30	35			
GGA GTA TTC	TGT AAT GAT	GAG TCC ATC	AAG TAC CCT	TAC AAA GAA	GAC	497
Gly Val Phe	Cys Asn Asp	Glu Ser Ile	Lys Tyr Pro	Tyr Lys Glu	Asp	
	40	45	50			
ACC ATA CCT	TAT GCG TTA	TTA GGT GGA	ATA ATC ATT	CCA TTC AGT	ATT	545
Thr Ile Pro	Tyr Ala Leu	Leu Leu Gly	Gly Ile Ile	Ile Pro Phe	Ser Ile	
	55	60	65			
ATC GTT ATT	ATT CTT GGA	GAA ACC CTG	TCT GTT TAC	TGT AAC CTT	TTG	593
Ile Val Ile	Ile Leu Gly	Glu Thr Leu	Ser Val Tyr	Cys Asn Leu	Leu	
70	75	80				
CAC TCA AAT	TCC TTT ATC	AGG AAT AAC	TAC ATA GCC	ACT ATT TAC	AAA	641
His Ser Asn	Ser Phe Ile	Arg Asn Asn	Tyr Ile Ala	Thr Ile Tyr	Lys	
85	90	95	100			
GCC ATT GGA	ACC TTT TTA	TTT GGT GCA	GCT GCT AGT	CAG TCC CTG	ACT	689
Ala Ile Gly	Thr Phe Leu	Phe Gly Ala	Ala Ala Ser	Gln Ser Leu	Thr	
	105	110	115			
GAC ATT GCC	AAG TAT TCA	ATA GGC AGA	CTG CGG CCT	CAC TTC TTG	GAT	737
Asp Ile Ala	Lys Tyr Ser	Ile Gly Arg	Leu Arg Pro	His Phe Leu	Asp	
	120	125	130			
GTT TGT GAT	CCA GAT TGG	TCA AAA ATC	AAC TGC AGC	GAT GGT TAC	ATT	785
Val Cys Asp	Pro Asp Trp	Ser Lys Ile	Asn Cys Ser	Asp Gly Tyr	Ile	
	135	140	145			
GAA TAC TAC	ATA TGT CGA	GGG AAT GCA	GAA AGA GTT	AAG GAA GGC	AGG	833
Glu Tyr Tyr	Ile Cys Arg	Gly Asn Ala	Glu Arg Val	Lys Glu Gly	Arg	
150	155	160				
TTG TCC TTC	TAT TCA GGC	CAC TCT TCG	TTT TCC ATG	TAC TGC ATG	CTG	881
Leu Ser Phe	Tyr Ser Gly	His Ser Ser	Phe Ser Met	Tyr Cys Met	Leu	
165	170	175	180			
TTT GTG GCA	CTT TAT CTT	CAA GCC AGG	ATG AAG GGA	GAC TGG GCA	AGA	929
Phe Val Ala	Leu Tyr Leu	Gln Ala Arg	Met Lys Gly	Asp Trp Ala	Arg	
	185	190	195			
CTC TTA CGC	CCC ACA CTG	CAA TTT GGT	CTT GTT GCC	GTA TCC ATT	TAT	977
Leu Leu Arg	Pro Thr Leu	Gln Phe Gly	Leu Val Ala	Val Ser Ile	Tyr	
	200	205	210			
GTG GGC CTT	TCT CGA GTT	TCT GAT TAT	AAA CAC CAC	TGG AGC GAT	GTG	1025
Val Gly Leu	Ser Arg Val	Ser Asp Tyr	Lys His His	Trp Ser Asp	Val	
215	220	225				

TTG ACT GGA CTC ATT CAG GGA GCT CTG GTT GCA ATA TTA GTT GCT GTA Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val 230 235 240	1073
TAT GTA TCG GAT TTC TTC AAA GAA AGA ACT TCT TTT AAA GAA AGA AAA Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys 245 250 255 260	1121
GAG GAG GAC TCT CAT ACA ACT CTG CAT GAA ACA CCA ACA ACT GGG AAT Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn 265 270 275	1169
CAC TAT CCG AGC AAT CAC CAG CCT TGAAAGGCAG CAGGGTGCCC AGGTGAAGCT His Tyr Pro Ser Asn His Gln Pro 280	1223
GGCCTGTTTT CTAAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT TTCTTCCTGG	1283
TGTACAAGCC TTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA CTTTGTGTGT	1343
ACATAGTTAC CTTTAACTCA GTGTTATCT AATAGCTCTA AACTCATTAA AAAAAGCTCCA	1403
AGCCTTCCAC CAAAACAGTG CCCACCTGT ATACATTTTT ATTAACAAAAA TGTAATGCTT	1463
ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTTAA ATATAATACA	1523
TATTAATAATG TATGGGAGAA CCAACAAAAA AAAAAA	1563

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys 1 5 10 15
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr 20 25 30
Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro 35 40 45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile 50 55 60
Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr 65 70 75 80
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala 85 90 95
Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ser 100 105 110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro 115 120 125
His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser 130 135 140

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
 145 150 155 160
 Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
 165 170 175
 Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
 180 185 190
 Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
 195 200 205
 Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
 210 215 220
 Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
 225 230 235 240
 Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
 245 250 255
 Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
 260 265 270
 Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1566 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 342..1196

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGCTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCCG GGCTGGCACA CGAGCGCCTC GGCCTAACC	120
GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC	180
CGCCCCGTCT CAGCCCCGCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC	240
GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA	300
CCTCATTTCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG	353
Met Phe Asp Lys	
1	
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
5 10 15 20	

TCC	ATG	CCT	ATG	GCT	GTT	CTA	AAA	TTG	GGC	CAA	ATA	TAT	CCA	TTT	CAG	449
Ser	Met	Pro	Met	25	Ala	Val	Leu	Lys	Leu	30	Gln	Ile	Tyr	Pro	Phe	Gln
AGA	GGC	TTT	TTC	TGT	AAA	GAC	AAC	AGC	ATC	AAC	TAT	CCG	TAC	CAT	GAC	497
Arg	Gly	Phe	Phe	40	Cys	Lys	Asp	Asn	45	Ser	Ile	Asn	Tyr	Pro	Tyr	His
AGT	ACC	GCC	GCA	TCC	ACT	GTC	CTC	ATC	CTA	GTG	GGG	GTT	GGC	TTG	CCC	545
Ser	Thr	Ala	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly	Val	Gly	Leu	Pro
GTT	TCC	TCT	ATT	ATT	CTT	GGA	GAA	ACC	CTG	TCT	GTT	TAC	TGT	AAC	CTT	593
Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	Tyr	Cys	Asn	Leu	
TTG	CAC	TCA	AAT	TCC	TTT	ATC	AGT	AAT	AAC	TAC	ATA	GCC	ACT	ATT	TAC	641
Leu	His	Ser	Asn	Ser	90	Phe	Ile	Ser	Asn	Asn	95	Ile	Ala	Thr	Ile	Tyr
AAA	GCC	ATT	GGA	ACC	TTT	TTA	TTT	GGT	GCA	GCT	GCT	AGT	CAG	TCC	CTG	689
Lys	Ala	Ile	Gly	105	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ser	Gln	Ser	Leu	
ACT	GAC	ATT	GCC	AAG	TAT	TCA	ATA	GGC	AGA	CTG	CGG	CCT	CAC	TTC	TTG	737
Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	
GAT	GTT	TGT	GAT	CCA	GAT	TGG	TCA	AAA	ATC	AAC	TGC	AGC	GAT	GGT	TAC	785
Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	Asp	Gly	Tyr	
ATT	GAA	TAC	TAC	ATA	TGT	CGA	GGG	AAT	GCA	GAA	AGA	GTT	AAG	GAA	GGC	833
Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	Val	Lys	Glu	Gly	
AGG	TTG	TCC	TTC	TAT	TCA	GGC	CAC	TCT	TCG	TTT	TCC	ATG	TAC	TGC	ATG	881
Arg	Leu	Ser	Phe	Tyr	170	Gly	His	Ser	Ser	175	Ser	Met	Tyr	Cys	Met	
CTG	TTT	GTG	GCA	CTT	TAT	CTT	CAA	GCC	AGG	ATG	AAG	GGA	GAC	TGG	GCA	929
Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	Asp	Trp	Ala	
AGA	CTC	TTA	CGC	CCC	ACA	CTG	CAA	TTT	GGT	CTT	GTT	GCC	GTA	TCC	ATT	977
Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	Ala	Val	Ser	Ile	
TAT	GTG	GGC	CTT	TCT	CGA	GTT	TCT	GAT	TAT	AAA	CAC	CAC	TGG	AGC	GAT	1025
Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	Trp	Ser	Asp	
GTG	TTG	ACT	GGA	CTC	ATT	CAG	GGA	GCT	CTG	GTT	GCA	ATA	TTA	GTT	GCT	1073
Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala	Ile	Leu	Val	Ala	
GTA	TAT	GTA	TCG	GAT	TTC	TTC	AAA	GAA	AGA	ACT	TCT	TTT	AAA	GAA	AGA	1121
Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser	Phe	Lys	Glu	Arg	
AAA	GAG	GAG	GAC	TCT	CAT	ACA	ACT	CTG	CAT	GAA	ACA	CCA	ACA	ACT	GGG	1169
Lys	Glu	Glu	Asp	265	Ser	His	Thr	Thr	Leu	His	Glu	Thr	Pro	Thr	Thr	Gly
AAT	CAC	TAT	CCG	AGC	AAT	CAC	CAG	CCT	TGAAAGGCAG	CAGGGTGCCC						1216
Asn	His	Tyr	280	Ser	Asn	His	Gln	Pro	285							

AGGTGAAGCT GGCCTGTTTT CTAAGGAAA ATGATTGCCA CAAGGCAAGA GGATGCATCT	1276
TTCTTCTCGG TGTACAAGCC TTTAAAGACT TCTGCTGCTG ATATGCCTCT TGGATGCACA	1336
CTTTGTGTGT ACATAGTTAC CTTTAACTCA GTGGTTATCT AATAGCTCTA AACTCATTAA	1396
AAAAACTCCA AGCCTTCCAC CAAAACAGTG CCCACCTGT ATACATTTTT ATTAATAAAAA	1456
TGTAATGCTT ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTAA	1516
ATATAATACA TATTAATAATG TATGGGAGAA CCAAAAAAAA AAAAAAAA	1566

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys
1				5					10					15	
Val	Leu	Leu	Ala	Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile
			20					25					30		
Tyr	Pro	Phe	Gln	Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr
		35				40						45			
Pro	Tyr	His	Asp	Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly
	50				55						60				
Val	Gly	Leu	Pro	Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val
	65				70					75					80
Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Ser	Asn	Asn	Tyr	Ile
			85						90					95	
Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala
			100					105					110		
Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg
		115					120					125			
Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys
	130					135				140					
Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg
	145				150				155					160	
Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser
			165						170					175	
Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys
			180					185					190		
Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val
		195					200					205			
Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His
	210					215					220				

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
 225 230 235 240
 Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
 245 250 255
 Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
 260 265 270
 Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
 275 280 285

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 294..1226

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTCCCCCTTG GACTTTAGAA 60
 CGATTTAGGG TTGACAGAGG AAAGCAGAGG CGCGCAGGAG GAGCAGAAAA CACCACCTTC 120
 TGCAATTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG 180
 ACCCGCCACT ATCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCCCTG GGTGTGTGGC 240
 TGTGTGTGCG GGACGCTCTC GCGGGGCGGG AGGCTCGCGC CGCAGCCAGC GCC ATG 296
 Met
 1
 CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC 344
 Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly
 5 10 15
 GGC AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG 392
 Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg
 20 25 30
 GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC 440
 Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu
 35 40 45
 CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG 488
 Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly
 50 55 60 65
 TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG 536
 Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu
 70 75 80

ACA ATA AAT GAC GCT GTG CTC TGT GCC GTG GGG ATC GTC ATT GCC ATC	584
Thr Ile Asn Asp Ala Val Leu Cys 85 90 Val Gly Ile Val Ile Ala Ile	
CTC GCG ATC ATC ACG GGG GAA TTC TAC CGG ATC TAT TAC CTG AAG AAG	632
Leu Ala Ile Ile Thr Gly Glu Phe 100 105 Tyr Arg Ile Tyr Leu Lys Lys	
TCG CGG TCG ACG ATT CAG AAC CCC TAC GTG GCA GCA CTC TAT AAG CAA	680
Ser Arg Ser Thr Ile Gln Asn Pro 115 120 Tyr Val Ala Ala Leu Tyr Lys Gln	
GTG GGC TGC TTC CTC TTT GGC GGC ATC AGC CAG TCT TTC ACA GAC	728
Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr Asp 130 135 140 145	
ATT GCC AAA GTG TCC ATA GGG CGC CTG CGT CCT CAC TTC TTG AGT GTC	776
Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser Val 150 155 160	
TGC AAC CCT GAT TTC AGC CAG ATC AAC TGC TCT GAA GGC TAC ATT CAG	824
Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile Gln 165 170 175	
AAC TAC AGA TGC AGA GGT GAT GAC AGC AAA GTC CAG GAA GCC AGG AAG	872
Asn Tyr Arg Cys Arg Gly Asp Ser Lys Val Gln Ala Arg Lys 180 185 190	
TCC TTC TTC TCT GGC CAT GCC TCC TTC TCC ATG TAC ACT ATG CTG TAT	920
Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu Tyr 195 200 205	
TTG GTG CTA TAC CTG CAG GCC CGC TTC ACT TGG CGA GGA GCC CGC CTG	968
Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg Leu 210 215 220 225	
CTC CGG CCC CTC CTG CAG TTC ACC TTG ATC ATG ATG GCC TTC TAC ACG	1016
Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr Thr 230 235 240	
GGA CTG TCT CGC GTA TCA GAC CAC AAG CAC CAT CCC AGT GAT GTT CTG	1064
Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val Leu 245 250 255	
GCA GGA TTT GCT CAA GGA GCC CTG GTG GCC TGC TGC ATA GTT TTC TTC	1112
Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe Phe 260 265 270	
GTG TCT GAC CTC TTC AAG ACT AAG ACG ACG CTC TCC CTG CCT GCC CCT	1160
Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala Pro 275 280 285	
GCT ATC CGG AAG GAA ATC CTT TCA CCT GTG GAC ATT ATT GAC AGG AAC	1208
Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg Asn 290 295 300 305	
AAT CAC CAC AAC ATG ATG TAGGTGCCAC CCACCTCCTG AGCTGTTTTT	1256
Asn His His Asn Met Met 310	
GTAAATGAC TGCTGACAGC AAGTTCCTGC TGCTCTCCAA TCTCATCAGA CAGTAGAATG	1316
TAGGGAAGAAA CTTTTGCCCG ACTGATTTTT AAAAAAAAAA AAAAAA	1362

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn
 1          5          10
Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys
          20          25          30
Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly
          35          40          45
Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg
          50          55          60
Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly
          65          70          75          80
Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala
          85          90          95
Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys
          100          105          110
Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys
          115          120          125
Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr
          130          135          140
Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser
          145          150          155          160
Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile
          165          170          175
Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg
          180          185          190
Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu
          195          200          205
Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg
          210          215          220
Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr
          225          230          235          240
Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val
          245          250          255
Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe
          260          265          270
Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala
          275          280          285
Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg
          290          295          300

```

Asn Asn His His Asn Met Met
305 310

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..833

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTG CTG TGC TTA	48
Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu	
1 5 10 15	
CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC GCC CCG	96
Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro	
20 25 30	
TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG TAC CCC TAC	144
Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr	
35 40 45	
CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG GTC ACC ATC ACG	192
Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr	
50 55 60	
GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC TAC CTG GTG TAC ACA	240
Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr	
65 70 75	
GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC AAC TAC GTG GCT GCT GTA	288
Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val	
80 85 90 95	
TAC AAG GTG CTG GGG ACC TTC CTG TTT GGG GCT GCC GTG AGC CAG TCT	336
Tyr Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser	
100 105 110	
CTG ACA GAC CTG GCC AAG TAC ATG ATT GGG CGT CTG AAG CCC AAC TTC	384
Leu Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe	
115 120 125	
CTA GCC GTC TGC GAC CCC GAC TGG AGC CGG GTC AAC TGC TCG GTC TAT	432
Leu Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr	
130 135 140	
GTG CAG CTG GAG AAG GTG TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG	480
Val Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu	
145 150 155	
GCC AGG TTG TCT TTC TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC	528
Ala Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys	
160 165 170 175	

ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG	576
Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp	
180 185 190	
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC	624
Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala	
195 200 205	
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC	672
Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser	
210 215 220	
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT	720
Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	
225 230 235	
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT	768
Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys	
240 245 250 255	
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG	816
Leu Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu	
260 265 270	
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC	863
Thr Leu Gly Arg Gly	
275	
TTCTTCTGA GGCCGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCCA	923
CCCAGGTGGT CCCTCCAGCC TGGTTAGGCA CTGAGGGTTC TGGACGGGCT CCAGGAACCC	983
TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC	1043
TGGAGATGCC TGGGTAGCCC TCAGCATTG GAGGGGAACC TGTTCCTGC GGTCCCCAAA	1103
TATCCCTTC TTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTTG	1163
TAAATGTAA TGTATATGTG GTTTTATAGTA AATAGGGCA CCTGTTTCAC AAAAAAAAAA	1223
AAAAAAAAA	1232

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu	Leu
1					5					10				15	
Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	Tyr
		20					25						30		
Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	Tyr	Pro	Tyr	Arg
		35				40					45				
Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	Val	Thr	Ile	Thr	Ala
	50					55					60				

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
65 70 75 80
Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
85 90 95
Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
100 105 110
Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
115 120 125
Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
130 135 140
Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
145 150 155 160
Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
165 170 175
Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
180 185 190
Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
195 200 205
Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His Trp Ser Asp
210 215 220
Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
225 230 235 240
Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
245 250 255
Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
260 265 270
Leu Gly Arg Gly
275

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys
1 5 10 15
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
20 25 30
Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro
35 40 45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile
50 55 60

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Pro Phe Cys Ile Ile Val Met Ser Ile Gly Glu Ser Leu Ser Val Tyr
65      70      75
Phe Asn Val Leu His Ser Asn Ser Phe Val Gly Asn Pro Tyr Ile Ala
85      90      95
Thr Ile Tyr Lys Ala Val Gly Ala Phe Leu Phe Gly Val Ser Ala Ser
100      105      110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Thr Ile Gly Ser Leu Arg Pro
115      120      125
His Phe Leu Ala Ile Cys Asn Pro Asp Trp Ser Lys Ile Asn Cys Ser
130      135      140
Asp Gly Tyr Ile Glu Asp Tyr Ile Cys Gln Gly Asn Glu Glu Lys Val
145      150      155      160
Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
165      170      175
Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
180      185      190
Asp Trp Ala Arg Leu Leu Arg Pro Met Leu Gln Phe Gly Leu Ile Ala
195      200      205
Phe Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
210      215      220
Trp Ser Asp Val Thr Val Gly Leu Ile Gln Gly Ala Ala Met Ala Ile
225      230      235      240
Leu Val Ala Leu Tyr Val Ser Asp Phe Phe Lys Asp Thr His Ser Tyr
245      250      255
Lys Glu Arg Lys Glu Glu Asp Pro His Thr Thr Leu His Glu Thr Ala
260      265      270
Ser Ser Arg Asn Tyr Ser Thr Asn His Glu Pro
275      280

```

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
1      5      10
Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
20      25      30
Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro
35      40      45
Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile
50      55      60

```

```

Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr
65          70          75          80
Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala
          85          90          95
Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser
          100          105          110
Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro
          115          120          125
His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser
          130          135          140
Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
          145          150          155          160
Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
          165          170          175
Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
          180          185          190
Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
          195          200          205
Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
          210          215          220
Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
          225          230          235          240
Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
          245          250          255
Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
          260          265          270
Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
          275          280

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
1          5          10          15
Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile
          20          25          30
Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr
          35          40          45
Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly
          50          55          60

```

Val	Gly	Leu	Pro	Val	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val
65					70				75					80
Tyr	Cys	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arg	Asn	Asn	Tyr
				85					90					95
Ala	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala
				100				105					110	
Ser	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu
				115			120					125		Arg
Pro	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn
				130		135					140			Cys
Ser	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu
145					150					155				160
Val	Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe
				165					170					175
Met	Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met
			180					185					190	Lys
Gly	Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu
			195				200					205		Val
Ala	Val	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys
			210			215					220			His
His	Trp	Ser	Asp	Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val
225				230						235				240
Ile	Leu	Val	Ala	Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr
				245					250				255	Ser
Phe	Lys	Glu	Arg	Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu
			260				265						270	Thr
Pro	Thr	Thr	Gly	Asn	His	Tyr	Pro	Ser	Asn	His	Gln	Pro		
			275				280					285		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Gln	Asn	Tyr	Lys	Tyr	Asp	Lys	Ala	Ile	Val	Pro	Glu	Ser	Lys	Asn
1				5					10					15	
Gly	Gly	Ser	Pro	Ala	Leu	Asn	Asn	Asn	Pro	Arg	Arg	Ser	Gly	Ser	Lys
			20					25					30		
Arg	Val	Leu	Leu	Ile	Cys	Leu	Asp	Leu	Phe	Cys	Leu	Phe	Met	Ala	Gly
			35				40					45			
Leu	Pro	Phe	Leu	Ile	Ile	Glu	Thr	Ser	Thr	Ile	Lys	Pro	Tyr	His	Arg
			50			55					60				

Gly	Phe	Tyr	Cys	Asn	Asp	Glu	Ser	Ile	Lys	Tyr	Pro	Leu	Lys	Thr	Gly	65	70	75	80
Glu	Thr	Ile	Asn	Asp	Ala	Val	Leu	Cys	Ala	Val	Gly	Ile	Val	Ile	Ala	85	90	95	
Ile	Leu	Ala	Ile	Ile	Thr	Gly	Glu	Phe	Tyr	Arg	Ile	Tyr	Tyr	Leu	Lys	100	105	110	
Lys	Ser	Arg	Ser	Thr	Ile	Gln	Asn	Pro	Tyr	Val	Ala	Ala	Leu	Tyr	Lys	115	120	125	
Gln	Val	Gly	Cys	Phe	Leu	Phe	Gly	Cys	Ala	Ile	Ser	Gln	Ser	Phe	Thr	130	135	140	
Asp	Ile	Ala	Lys	Val	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	Ser	145	150	155	160
Val	Cys	Asn	Pro	Asp	Phe	Ser	Gln	Ile	Asn	Cys	Ser	Glu	Gly	Tyr	Ile	165	170	175	
Gln	Asn	Tyr	Arg	Cys	Arg	Gly	Asp	Asp	Ser	Lys	Val	Gln	Glu	Ala	Arg	180	185	190	
Lys	Ser	Phe	Phe	Ser	Gly	His	Ala	Ser	Phe	Ser	Met	Tyr	Thr	Met	Leu	195	200	205	
Tyr	Leu	Val	Leu	Tyr	Leu	Gln	Ala	Arg	Phe	Thr	Trp	Arg	Gly	Ala	Arg	210	215	220	
Leu	Leu	Arg	Pro	Leu	Leu	Gln	Phe	Thr	Leu	Ile	Met	Met	Ala	Phe	Tyr	225	230	235	240
Thr	Gly	Leu	Ser	Arg	Val	Ser	Asp	His	Lys	His	His	Pro	Ser	Asp	Val	245	250	255	
Leu	Ala	Gly	Phe	Ala	Gln	Gly	Ala	Leu	Val	Ala	Cys	Cys	Ile	Val	Phe	260	265	270	
Phe	Val	Ser	Asp	Leu	Phe	Lys	Thr	Lys	Thr	Thr	Leu	Ser	Leu	Pro	Ala	275	280	285	
Pro	Ala	Ile	Arg	Lys	Glu	Ile	Leu	Ser	Pro	Val	Asp	Ile	Ile	Asp	Arg	290	295	300	
Asn	Asn	His	His	Asn	Met	Met										305	310		

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu	Leu	1	5	10	15
Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	Tyr	20	25	30	

Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg
 35 40 45
 Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala
 50 55 60
 Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp
 65 70 75 80
 Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr
 85 90 95
 Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu
 100 105 110
 Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu
 115 120 125
 Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val
 130 135 140
 Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala
 145 150 155 160
 Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met
 165 170 175
 Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala
 180 185 190
 Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu
 195 200 205
 Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp
 210 215 220
 Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val
 225 230 235 240
 Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu
 245 250 255
 Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr
 260 265 270
 Leu Gly Arg Gly
 275

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCTAGAT ATTAAATAGTA ATCAATTAC

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCATGCG TGAGGCTCCG GTGC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAGTTTTC ACGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTTTCG AAGACGCGGC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATATGTAGT ATTCAATGTA ACC

23

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGATGGCTAG CATGCAGAGA AGATGGGTCT TCGTGCTGCT CGACGTG

47

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGTGCGGGAT CCCATAAGTG GTTG

24

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 077319/0125

In re patent application of

David W. LEUNG et al.

Serial No. 08/842,827

Group Art Unit: 1801

Filed: April 17, 1997

Examiner: Unassigned

For: HUMAN PHOSPHATIDIC ACID PHOSPHATASE

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In response to the Notice to Comply With Requirements for Applications Containing Sequence Disclosures mailed June 9, 1997, please amend the application as follows:

IN THE SPECIFICATION:

Page 3, line 22, after "284" insert --(SEQ ID NO:2)--;
line 24, after "285" insert --(SEQ ID NO:4)--;
line 25, after "276" insert --(SEQ ID NO:8)--;
line 30, after "284" insert --(SEQ ID NO:2)--;
line 31, after "285" insert --(SEQ ID NO:4)--;
line 33, after "276" insert --(SEQ ID NO:8)--.

Page 4, line 23, after "sequence" insert --(SEQ ID NOS:1 and 2)--;
line 26, after "sequence" insert --(SEQ ID NOS:3 and 4)--;
line 29, after "sequence" insert --(SEQ ID NOS:5 and 6)--;
line 32, after "sequence" insert --(SEQ ID NOS:7 and 8)--;

Serial No. 08/842,827

line 33, after "sequences" insert --(SEQ ID NOS:9-13)--.

Page 7, line 35, after "4" insert --(SEQ ID NOS:2, 4, 6 and 8)--.

Page 10, line 18, after "1193" insert --of SEQ ID NO:1--;

line 19, after "1196" insert --of SEQ ID NO:3--; delete "amino acid number";

line 20, delete "1 to amino acid number 311" and insert --nucleotide number 294 to nucleotide number 1226 of SEQ ID NO:5--;

line 21, after "833" insert --of SEQ ID NO:7--.

Page 11, line 12, after "4" insert --(SEQ ID NOS:1, 3, 5 and 7)--.

Page 14, line 31, after "3'" insert --(SEQ ID NO:14)--;
line 32, after "3'" insert --(SEQ ID NO:15)--;
line 36, after "3'" insert --(SEQ ID NO:16)--.

Page 15, line 1, after "3'" insert --(SEQ ID NO:17)--.

Page 18, line 34, after "3'" insert --(SEQ ID NO:18)--;
line 35, after "3'" insert --(SEQ ID NO:19)--.

Page 19, line 25, after "3'" insert --(SEQ ID NO:14)--;
line 26, after "3'" insert --(SEQ ID NO:15)--;
line 30, after "3'" insert --(SEQ ID NO:16)--;
line 31, after "3'" insert --(SEQ ID NO:17)--.

Page 20, line 4, after "3'" insert --(SEQ ID NO:20)--;
line 6, after "3'" insert --(SEQ ID NO:21)--;

Serial No. 08/842,827

line 15, before "respectively" insert --(SEQ ID NOS:1, 3, 5 and 7)--;

line 21, after "4" insert --, SEQ ID NOS:2, 4, 6 and 8--.

Page 22, at the end of the specification, before the claims, insert the printed Sequence Listing submitted concurrently herewith, and renumber pages 1-19 of the Sequence Listing as pages 23-41 of the specification.

IN THE CLAIMS:

Please renumber pages 23-24 as pages 42-43 and amend the claims as follows.

1. (Amended) An isolated polynucleotide encoding human phosphatidic acid phosphatase wherein said polynucleotide encodes a protein comprising a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

2. (Amended) An isolated human phosphatidic acid phosphatase protein, wherein said protein comprises a polypeptide sequence selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), and (iii) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

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4. (Amended) The method of claim 3, wherein said polynucleotide encoding human phosphatidic acid is selected from the group consisting of (i) the sequence at amino acid number 1 to amino acid number 284 in Figure 1 (SEQ ID NO:2), (ii) the sequence at amino acid number 1 to amino acid number 285 in Figure 2 (SEQ ID NO:4), (iii) the sequence at amino acid number 1 to amino acid number 311 in Figure 3 (SEQ ID NO:6), and (iv) the sequence at amino acid number 1 to amino acid number 276 in Figure 4 (SEQ ID NO:8).

Claim 6, line 3, after "1" insert --(SEQ ID NO:2)--.

Claim 7, line 3, after "2" insert --(SEQ ID NO:4)--.

Claim 8, line 3, after "3" insert --(SEQ ID NO:6)--.

Claim 9, line 3, after "4" insert --(SEQ ID NO:8)--.

REMARKS

Applicants submit this Preliminary Amendment to insert required references to SEQ ID NOS of the Sequence Listing filed concurrently herewith, to indicate the insertion point for the Sequence Listing, and to effect the necessary changes in pagination. Applicants also have corrected a typographical error appearing at page 10, lines 19-20. Applicants respectfully request examination on the merits of this application.

It is believed that no additional fees are required; however, the Commissioner is hereby authorized to charge any deficiency or credit any overpayment to Deposit Account No. 19-0741. It is further believed that no additional petition for an extension of time under 37 C.F.R. § 1.136 is required. However, should such a petition be required, applicant hereby petitions the Commissioner for an extension of time, and authorizes the Commissioner to charge the necessary petition fee to Deposit Account No. 19-0741.

Respectfully submitted,

5 August 1997
Date

S. A. Bent
Stephen A. Bent
Reg. No. 29,768

FOLEY & LARDNER
Suite 500
3000 K Street, NW
Washington, D.C. 20007-5109
(202) 672-5300



DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address, and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

HUMAN PHOSPHATIDIC ACID PHOSPHATASE

the specification of which is attached hereto unless the following box is checked:

☒ was filed on April 17, 1997 as United States Application Number or PCT International Application Number 08/842,827
and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed:

PRIOR FOREIGN APPLICATION(S)

NUMBER	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

APPLICATION NO.	FILING DATE


I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is known by me to be material to patentability as defined in Title 37, Code of Federal Regulations § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

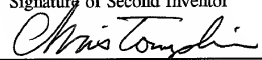
APPLICATION SERIAL NO.	FILING DATE	STATUS: PATENTED, PENDING, ABANDONED

I hereby appoint as my attorneys, with full powers of substitution and revocation, to prosecute this application and transact all business in the Patent and Trademark Office connected therewith: Stephen A. Bent, Reg. No. 29,768; David A. Blumenthal, Reg. No. 26,257; William T. Ellis, Reg. No. 26,874; John J. Feldhaus, Reg. No. 28,822; Patricia D. Granados, Reg. No. 33,683; John P. Isacson, Reg. No. 33,715; Donald D. Jeffery, Reg. No. 19,980; Eugene M. Lee, Reg. No. 32,039; Peter G. Mack, Reg. No. 26,001; Brian J. McNamara, Reg. No. 32,789; Sybil Meloy, Reg. No. 22,749; George E. Quillin, Reg. No. 32,792; Colin G. Sandercock, Reg. No. 31,298; Bernhard D. Saxe, Reg. No. 28,665; Charles F. Schill, Reg. No. 27,590; Richard L. Schwaab, Reg. No. 25,479; Arthur Schwartz, Reg. No. 22,115; Harold C. Wegner, Reg. No. 25,258.

Address all correspondence to **FOLEY & LARDNER**, 3000 K Street, N.W., Suite 500, P.O. Box 25696, Washington, D.C. 20007-8696.
Address telephone communications to John P. Isacson at (202) 672-5300.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of First or Sole Inventor <u>David W. LEUNG</u> 1-00	Signature of First or Sole Inventor 	Date 7/16/97
Residence Address <u>Mercer Island, Washington</u> WA	Country of Citizenship USA	
Post Office Address 7625 E. Mercer Way, Mercer Island, Washington 98040		

Full Name of Second Inventor <u>Christopher K. TOMPKINS</u> 2-00	Signature of Second Inventor 	Date 7/16/97
Residence Address <u>Bothell, Washington</u> WA	Country of Citizenship USA	
Post Office Address 17660 86th Avenue, N.E., Bothell, Washington 98011		

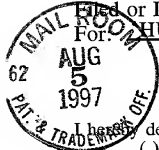
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Applicant or Patentee: David W. LEUNG et al

Serial or Patent No.: 08/842,827

Atty. Dkt. No. 077319/0125

Filed or Issued: April 17, 1997



HUMAN PHOSPHATIDIC ACID PHOSPHATASE

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) AND 1.27 (c)) — SMALL BUSINESS CONCERN

I hereby declare that I am

☐ the owner of the small business concern identified below:

☐ an official of the small business concern empowered to act on behalf of the concern identified below:

NAME OF CONCERN CELL THERAPEUTICS, INC.

ADDRESS OF CONCERN Suite #401, 201 Elliott Avenue, West, Seattle, Washington, 98119

I hereby declare that the above-identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18 and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled HUMAN PHOSPHATIDIC ACID PHOSPHATASE by inventor(s) David W. LEUNG et al. described in

☐ the specification filed herewith

☒ application serial no. 08/842,827, filed April 17, 1997

☐ patent no. _____, issued _____

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(c) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). * NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities: (37 CFR 1.27)

NAME: _____

ADDRESS: _____

☐ INDIVIDUAL

☐ SMALL BUSINESS CONCERN

☐ NONPROFIT CORPORATION

NAME: _____

ADDRESS: _____

☐ INDIVIDUAL

☐ SMALL BUSINESS CONCERN

☐ NONPROFIT CORPORATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate: (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Maurice J. Schwarz, PhD

TITLE OF PERSON OTHER THAN OWNER: EVP, Product Development

ADDRESS OF PERSON SIGNING: 201 Elliott Avenue West, Suite 400, Seattle, WA 98119

SIGNATURE: _____

DATE: 7/16/97